

GenCore version 4.5
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OM protein - protein search, using sw model.

Run on: March 1, 2001, 16:17:05 ; Search time 17.21 Seconds
(without alignments)

112.588 Million cell updates/sec

Title: US-09-331-631a-22_COPY_25_84
Perfect score: 350
Sequence: EDDNHHHGGHKGCGCVRRC.....EKROERSRHEADDRSGEGSS 60

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match Length DB ID

Description

Result No.	Score	Query Match	Length	DB ID	Description
1	346	98.9	573	1 GLBL_MAIZE	P15590 zea mays (m
2	81.5	23.3	605	1 VCLA_GOSHI	p09799 gossypium h
3	78	22.3	494	1 SFR4_HUMAN	Q08170 homo sapien
4	71	20.3	699	1 P23327_homo_sapien	P23327 homo sapien
5	69.5	19.9	241	1 YO87_CAEEL	P34623 caenorhabdi
6	69	19.7	407	1 IEE68_HSVA	Q01042 herpesvirus
7	69	19.7	588	1 VCLB_HUMAN	P09801 gossypium h
8	68.5	19.6	1407	1 TRHL_RABIT	P37709 oryctolagus
9	67.5	19.3	466	1 CYPB_CAEEL	P52016 caenorhabdi
10	66	18.9	2339	1 CCAB_HUMAN	Q09975 homo sapien
11	66	18.9	2339	1 CCAE_RABIT	Q05152 oryctolagus
12	65.5	18.7	345	1 VU79_HSVA2	P52530 herpes simp
13	65.5	18.7	520	1 ITSN_HUMAN	Q15811 homo sapien
14	65.5	18.7	2222	1 CCAC_RAT	Q07652 rattus norv
15	65.5	18.7	2272	1 CCAE_MOUSE	Q61290 mus musculus
16	65.5	18.7	2312	1 CCAE_HUMAN	Q15878 homo sapien
17	65	18.6	107	1 HSP2_MOUSE	P07978 mus musculus
18	65	18.6	1130	1 REPT_MOUSE	P97347 mus musculus
19	63.5	18.1	520	1 LEG2_PEA	P15838 pisum sativu
20	63.5	18.1	2505	1 CCAA_HUMAN	Q00555 homo sapien
21	63	18.0	311	1 OSTP_RABBIT	P33097 oryctolagus
22	63	18.0	330	1 RLX3_STAAU	P14491 staphylococ
23	63	18.0	344	1 SFR6_HUMAN	Q13247 homo sapien
24	63	18.0	380	1 RDP_HUMAN	P18615 homo sapien
25	63	18.0	467	1 RXRG_CHICK	P28701 gallus gallus
26	63	18.0	632	1 CCB2_RABBIT	P52288 oryctolagus
27	63	18.0	747	1 TPT5_ECOLI	Q00192 escherichia
28	62.5	17.9	103	1 HSP2_MACNE	P5298 macaca nem
29	62.5	17.9	517	1 LEGA_PEA	P02857 pistis sativ
30	62.5	17.9	520	1 GAG_HV2SB	P12450 human immun
31	62	17.7	524	1 SGP_SOY2NB	Q04672 glycine max
32	62	17.7	623	1 PNTL_DROME	P51022 drosophila
33					Q28527 mustela put

ALIGNMENTS

Query Match

Score 346; DB 1; Length 573;

RT protein, and localization of the gene to human chromosome 19 and mouse chromosome 7";
 RT Genomics 9:656-669(1991).
 RL -!- FUNCTION: HCP MAY PLAY A ROLE IN THE REGULATION OF CA(2+)
 CC SEQUESTRATION OR RELEASE IN THE SR OF SKELETAL AND CARDIAC
 CC MUSCLE.
 CC -!- SUBCELLULAR LOCATION: SARCOPLASMIC RETICULUM LUMEN.
 CC -!- SIMILARITY: STRONG; TO RABBIT HRC.
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 CC
 DR EMBL: M60052; AAA88071.1; -.
 DR MIM: 14205; -.
 DR Calcium-binding; Signal; Repeat; Polymorphism.
 FT SIGNAL 1 28
 FT CHAIN 29 699
 DOMAIN 193 204
 DOMAIN 246 261
 DOMAIN 106 365
 DOMAIN 180 213
 REPEAT 238 270
 REPEAT 295 318
 REPEAT 343 365
 DOMAIN 106 342
 REPEAT 106 121
 REPEAT 134 154
 REPEAT 155 177
 REPEAT 214 237
 REPEAT 271 294
 REPEAT 319 342
 DOMAIN 627 673
 VARIANT 96 96
 SQ SEQUENCE 699 AA; 80244 MW; 992EEDF012C61DD CRC64;
 Query Match 20.3%; Score 71; DB 1; Length 699;
 Best Local Similarity 24.2%; Pred. No. 3.5; Indels 34; Gaps 3;
 Matches 22; Conservative 7; Mismatches 28;
 QY 1 EDDNNHHHG-----GHKS-----GQCVRRCEDRPWH---- 26
 Db 413 EVPHHHHVPRPDEEVSAELGHQAFSHRSQHQDEETGHGORGSIKEMSHHPPGHTWK 472
 QY 27 ORPCCLEQCREERERKKRERSRHSHEADDRSGE 57
 Db 473 DRSHLRKDODSEEEKEERKEEDPGSHEEDDSE 503
 RESULT 5
 Y07_CAEEL STANDARD; PRT; 241 AA.
 ID Y087_CAEEL STANDARD; PRT; 241 AA.
 AC P34623;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE HYPOTHETICAL 28.5 KDA PROTEIN ZKI236.7 IN CHROMOSOME III.
 GN ZKI236.7
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdita; Rhabditoidea;
 OC Rhabditidae; Podocerinae; Caenorhabditis.
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2.
 RX MEDLINE-94150718; PubMed=7906398;
 RA Nicholas J., Cameron K.R., Coleman H., Newman C., Hones R.W.;
 RA "Analysis of nucleotide sequence of the rightmost 43 kbp of
 RT herpesvirus saimiri (HVS) I-DNA: general conservation of genetic
 RT organization between HVS and Epstein-Barr virus.";
 RL Virology 188:296-310(1992).
 CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 AND
 CC HSV-2 IE-68 (US1), EHV-1 65, EHV-4 (ORF4), PRV RSP40, AND VZV 63.
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 CC
 DR EMBL: L13200; AAA28188.1; -.
 DR WORLPEP: ZKL1236.7; CE00384.
 KW HYPOTHETICAL PROTEIN.
 SQ SEQUENCE 241 AA; 28541 MW; 610ECA6537159FA7 CRC64;
 Query Match 19.9%; Score 69.5; DB 1; Length 241;
 Best Local Similarity 41.9%; Pred. No. 1.9;
 Matches 18; Conservative 9; Mismatches 9; Indels 7; Gaps 2;
 QY 17 VRCEDRPWHQRCLGCREREKR--QERRHEADRSGE 57
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DB 65 MREYEVREVERKR---RREEEKKDRERAKEADEKAE 102
 DE IMMEDIATE-EARLY PROTEIN.
 GN 73 OR EGFL.
 OS Herpesvirus saimiri (strain 11).
 OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammapathoparvovirinae; Rhadinovirus.
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE-9233368; PubMed=13121287;
 RA Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
 RA Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
 RA Hones R.W.;
 RA "Primary structure of the herpesvirus saimiri genome.";
 RL J. Virol. 66:5047-5058(1992).
 RN [2]
 SEQUENCE FROM N.A.
 RX MEDLINE-9220228; PubMed=1314457;
 RA Nicholas J., Cameron K.R., Coleman H., Newman C., Hones R.W.;
 RA "Analysis of nucleotide sequence of the rightmost 43 kbp of
 RT herpesvirus saimiri (HVS) I-DNA: general conservation of genetic
 RT organization between HVS and Epstein-Barr virus.";
 RL Virology 188:296-310(1992).
 CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 AND
 CC HSV-2 IE-68 (US1), EHV-1 65, EHV-4 (ORF4), PRV RSP40, AND VZV 63.
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 CC

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DR EMBL: X44346; CAA45696 1; -
DR EMBL: M66409; AAM6149 1; -
DR PIR: G3813; EDB03;
DR PIR: S20244; S20244.
DR HSSP: P33041; 1A17.
KW Early protein
FT DOMAIN 60 241 GLU-RICH (ACIDIC).
SEQUENCE 407 AA: 46617 MW: FFD399CA82CE136C CRC64;

Query Match 19.7%; Score 69; DB 1; Length 407;
Best local similarity 45.7%; Pred. No. 3.4;
Matches 16; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

Qy 26 HQRRCL--EQCREEREKRQRSHEADRSSEG 58
||: | | | | : | : | | | : |||
Db 52 HQQQALTEERREVEEPEGEERERRGEEERBEGEG 86

RESULT 7

ID VCB_GOSHI	STANDARD:	PRT: 588 AA.
AC P0801;		
DT 01-MAR-1989 (Rel. 10, Created)		
DT 15-JUL-1999 (Rel. 38, Last sequence update)		
DE VICILIN C72 PRECURSOR (ALPHA-GLOBULIN B).		
OS Gossypium hirsutum (Upland cotton).		
OC EUkaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.		
RN [1]		
RP SEQUENCE FROM N.A.		
RA Chian C.A., Pyle J.B., Legocki A.B., Dure L. III;		
RT "Developmental biochemistry of cottonseed embryogenesis and germination. XVIII. cDNA and amino acid sequences of the members of the storage protein families";		
RT Plant Mol. Biol. 7:475-489(1986).		
RL -!- FUNCTION: SEED STORAGE PROTEIN.		
CC -!- SUBCELLULAR LOCATION: COTYLEDONARY BODIES.		
CC -!- SIMILARITY: TO OTHER 75 SEED STORAGE PROTEINS (PHASBOLIN, VICILIN, CONVICILIN, CONGLYCLININ, ETC.).		
CC -----		
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CC -----		
DR EMBL: M16911; AAA33071 1; -.		
DR HSSP: P50477; ICAX.		
DR INTERPRO; IPR01113; -.		
DR PF0056; Seedstorage7s; 1.		
FT SIGNAL 1 25 CHAIN 26 588 MW: VICTILIN C72.		
SQ SEQUENCE 588 AA: 69729 MW: 63E89B29AB8ADEB CRC64;		

Query Match 19.7%; Score 69; DB 1; Length 588;
Best local similarity 30.6%; Pred. No. 4.7;
Matches 15; Conservative 12; Mismatches 16; Indels 6; Gaps 3;

Qy 15 OCVRRC--EDRPHWRPRCLEQCREEEREK--RQERSRHEADRSSEG 58

Query Match 19.6%; Score 68.5; DB 1; Length 1407;
 Best Local Similarity 47.1%; Pred. No. 12;
 Matches 16; Conservative 8; Mismatches 9; Indels 1; Gaps 1;

Qy 15 OCVRRECDRWHQRERCLQCREEREKQERSR 48
 Db 1090 QQLRRERDRKFREEQELQI-E-RERERLRRQERAR 1122

RESULT 9
 CYP8.CAEL STANDARD PRT; 466 AA.

ID CYP8.CAEL
 AC P52016;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE PEPTIDYL PROLYL CIS-TRANS ISOMERASE 8 (EC 5.2.1.8) (PPIASE) (ROTAMASE)
 DE (CYCLOPHILIN-B).
 DE CYP-8 OR D1008.2.
 OS Caenorhabditis elegans.

OC Rhabditidae; Peloderrinae; Caenorhabditis.
 RN [1] Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 RN STRAIN=BRISTOL N2;
 RC MEDLINE=86276416; PubMed=8694762;
 RA Page A.P.; Macniven K.; Hengartner M.O.;
 RT "Cloning and biochemical characterization of the cyclophilin homologues from the free-living nematode *Caenorhabditis elegans*.";
 RL Biochem. J. 317:179-185(1996).
 RN [2] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Favello T.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
 CC --!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS.
 CC --!- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC --!- SIMILARITY: CONTAINS A CYCLOPHILIN-LIKE PPIASE DOMAIN.

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CC PF00160; prok_isomerase; 1.
 DR PR00153; CSAPPISMRASE.
 DR EMBL; U40938; AAA81696.1; -.
 DR HSSP; P05092; 3CYS.
 DR WORMPEP; D1009.2; CE04386.
 DR INTERPRO; IPR002130; -.
 DR PFAM; PF00160; prok_isomerase; 1.
 DR PR00153; CSAPPISMRASE.
 DR PROSITE; PS00170; CSA_PPIASE_1; 1.
 DR PROSITE; PS55072; CSA_PPIASE_2; 1.
 DR KW Isomerase; Rotamase; Multigene family.
 FT DOMAIN 1 177 PPIASE, CYCLOPHILIN-TYPE.
 FT DOMAIN 234 239 POLY-ARG.
 FT DOMAIN 419 423 POLY-ARG.
 FT DOMAIN 450 459 POLY-SER.
 SQ 466 AA; 53565 MN; 6E014ABA0E54BAF3 CRC64;

Query Match 19.3%; Score 67.5; DB 1; Length 466;
 Best Local Similarity 34.4%; Pred. No. 5.4;
 Matches 22; Conservative 7; Mismatches 26; Indels 9; Gaps 3;

Qy 1 EDDNNHHGGHKGKSGOCVRCEDRWH-ORPRCLQCREEREKQERSR-----RHEND 52
 Db 221 EKKRKDKHGKREKRRRSNDRGDRRSRSRSRDRNR-RDDRSGRDGVRGNERD 279

RESULT 10
 CCAB_HUMAN STANDARD PRT; 2339 AA.

ID CCAB_HUMAN
 AC 000975;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIT).

DE CACNA1B OR CACNL1AS OR CACNS.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.

RN [1] SEQUENCE FROM N.A. (ISOFORMS ALPHA-1B-1 AND ALPHA-1B-2).
 RP TISSUE=BRAIN;
 RC MEDLINE=92335886; PubMed=1321501;
 RA Williams M.E.; Brust P.F.; Feldman D.H.; Patthi S.; Simerson S.; Maroufi A.; McCue A.F.; Velicelebi G.; Ellis S.B.; Harpold M.M.; RT "Structure and functional expression of an omega-conotoxin-sensitive human N-type calcium channel.;"
 RL Science 257:389-395(1992).
 RN [2] SEQUENCE OF 1-94 FROM N.A.
 RP TISSUE=LONG FIBROBLAST;
 RC Kim D.S.; Jung H.H.; Park S.H.; Chin H.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 CC --!- FUNCTION: VOLTAGE SENSITIVE CALCIUM CHANNELS (VSCCs) MEDIATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1B GIVES RISE TO N-TYPE CALCIUM CURRENTS. N-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY OMEGA-CONOTOXIN-EGTA (OMEGA-CTX-GVIA) AND BY OMEGA-AGATOK-TIA (OMEGA-AGA-TIA). THEY ARE, HOWEVER, INSENSITIVE TO DIHYDROPTIDINES (DHP), AND OMEGA AGATOXIN-IVA (OMEGA AGA-IVA). CALCIUM CHANNELS CONTAINING ALPHA-1B SUBUNIT MAY PLAY A ROLE IN DIRECTED MIGRATION OF IMMATURE NEURONS.

CC --!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC --!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC --!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA-1B-1 (SHOWN HERE) AND ALPHA-1B-2; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC --!- TISSUE SPECIFICITY: ALPHA-1B-1 AND ALPHA-1B-2 ARE EXPRESSED IN THE CENTRAL NERVOUS SYSTEM, BUT NOT IN SKELETAL MUSCLE OR AORTA.

CC --!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC --!- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CCPK (BY SIMILARITY).

CC --!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHAI-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION THROUGHOUT THE BRAIN. HIGHEST LEVELS IN CORPUS STRIATUM AND MIDBRAIN.

-!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

-!- PTM: PHOSPHORYLATED IN VITRO BY CAM-KINASE II, CAPK, PKC AND CGPK (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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EMBL: D14157; BAA03202.1; -.

INTERPRO: IPR00536; -.

INTERPRO: IPR002077; -.

PFAM: PF00520; Ion_trans; 4.

PRINTS: PRO0167; CACHANNEL.

KW Ion1 channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family; Calcium-binding; Phosphorylation; ATP-binding.

REPEAT 82 359 I.

REPEAT 469 713 III.

REPEAT 1142 1424 IV.

REPEAT 1461 1714 IV.

DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 1 95 S1_OF_REPEAT_I (POTENTIAL).

FT TRANSMEM 96 114 S1_OF_REPEAT_I (POTENTIAL).

FT DOMAIN 115 132 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 133 152 S2_OF_REPEAT_I (POTENTIAL).

FT DOMAIN 153 163 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 164 183 S3_OF_REPEAT_I (POTENTIAL).

FT DOMAIN 184 187 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 188 206 S4_OF_REPEAT_I (POTENTIAL).

FT DOMAIN 207 225 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 226 245 S5_OF_REPEAT_I (POTENTIAL).

FT DOMAIN 246 331 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 332 356 S6_OF_REPEAT_I (POTENTIAL).

FT DOMAIN 357 483 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 484 502 S1_OF_REPEAT_II (POTENTIAL).

FT DOMAIN 503 517 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 518 537 S2_OF_REPEAT_II (POTENTIAL).

FT DOMAIN 538 545 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 546 563 S3_OF_REPEAT_II (POTENTIAL).

FT DOMAIN 564 574 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 575 593 S4_OF_REPEAT_II (POTENTIAL).

FT DOMAIN 594 612 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 613 632 S5_OF_REPEAT_II (POTENTIAL).

FT DOMAIN 633 685 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 686 710 S6_OF_REPEAT_II (POTENTIAL).

FT DOMAIN 711 1156 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1157 1174 S1_OF_REPEAT_III (POTENTIAL).

FT DOMAIN 1175 1210 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1191 1220 S2_OF_REPEAT_III (POTENTIAL).

FT DOMAIN 1211 1222 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1223 1228 S3_OF_REPEAT_III (POTENTIAL).

FT DOMAIN 1242 1251 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1252 1270 S4_OF_REPEAT_III (POTENTIAL).

FT DOMAIN 1271 1289 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1290 1309 S5_OF_REPEAT_III (POTENTIAL).

FT DOMAIN 1310 1396 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1397 1421 S6_OF_REPEAT_III (POTENTIAL).

FT DOMAIN 1422 1476 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1477 1495 S1_OF_REPEAT_IV (POTENTIAL).

FT DOMAIN 1496 1510 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1511 1530 S2_OF_REPEAT_IV (POTENTIAL).

FT DOMAIN 1531 1538 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1539 1557 S3_OF_REPEAT_IV (POTENTIAL).

FT DOMAIN 1558 1566 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1567 1585 S4_OF_REPEAT_IV (POTENTIAL).

FT DOMAIN 1586 1604 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 1605 1624 S5_OF_REPEAT_IV (POTENTIAL).

FT DOMAIN 1625 1686 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 1687 1711 S6_OF_REPEAT_IV (POTENTIAL).

FT DOMAIN 1712 2339 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 2051 2119 POLY-HIS.

FT DOMAIN 2119 2123 POLY-SER.

FT DOMAIN 2319 2324 POLY-GLY.

FT DOMAIN 379 459 BINDING_TO_THE_BETA_SUBUNIT (BY SIMILARITY).

FT NP_BIND 452 459 ATP (POTENTIAL).

FT SITE 314 314 CALCIUM_ION_SELECTIVITY_AND_PERMEABILITY (BY SIMILARITY).

FT SITE 663 663 CALCIUM_ION_SELECTIVITY_AND_PERMEABILITY (BY SIMILARITY).

FT SITE 1370 1370 CALCIUM_ION_SELECTIVITY_AND_PERMEABILITY (BY SIMILARITY).

FT SITE 1658 1658 CALCIUM_ION_SELECTIVITY_AND_PERMEABILITY (BY SIMILARITY).

FT MOD_RES 1722 1722 PHOSPHORYLATION_BY_CAPK (POTENTIAL).

FT CA_BIND 1740 1751 BY_SIMILARITY.

FT CARBOHYD 256 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 1566 1566 N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 1678 1678 N-LINKED (GLCNAC . .) (POTENTIAL).

FT SEQUENCE 2339 AA; 261178 MW; 0413DA93794CB34 CRC64;

Query Match 18.9% Score 66: DB 1; Length 2339;

Best Local Similarity 28.2%; Pred. No. 32; Gaps 5;

Matches 24; Conservative 7; Mismatches 14; Indels 40; Gaps 5;

QY 4 NHHHHGKGSKSGCVRREDRPHQRPCLEQ

Dy 2051 HHHHH-----RCHRR-RDR---KQRSLEKGPSLADTDAPDSTDVGPGLUPTGEGPPGC 2099

QY 36 REFERERKQERERSHADDRSGBGS 60

Dy 2100 R-RERERQERGRSQERQQSSSS 2123

Db 2100 R-RERERQERGRSQERQQSSSS 2123

RESULT 12

V079_HSV62 STANDARD; PRT; 345 AA.

ID V079_HSV62

AC P52530;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 34, Last sequence update)

DE PROTEIN U79.

GN U79 OR CB7R.

OS Herpes simplex virus (type 6 / strain Z29).

OC Herpes simplex viruses, no RNA stage; Herpesviridae; Betaherpesvirinae; Roseolovirus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96195263; PUBMED=6634027;

RA Lindquester G.J., Inoue N., Allen R.D., Castelli J.W., Stamley F.R., Danovich R.M.,

RA Frenkell N., Pellett P.E.,

RA "Restriction endonuclease mapping and molecular cloning of the human herpesvirus 6 variant B strain Z29 genome.",

RL Arch. Virol. 141:367-379(1996).

CC -!- FUNCTION: POSSIBLE REPPLICATION PROTEIN.

CC -!- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND HSV-7 U79 AND HCMV UL112 (P34).

DR	INTERPRO; IPR002077; -	PRT	SITE	1615	1615	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;	PRT	CA_BIND	377	389	BY SIMILARITY.
KW	Calcium channel; Glycoprotein; Repeat; Multigene family;	PRT	MOD_RES	1686	1686	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
KW	Calcium-binding; Phosphorylation.	PRT	CA_BIND	1704	1715	BY SIMILARITY.
REPEAT	27	PRT	CARBOHYD	205	205	N-LINKED (GLCNAC. . .) (POTENTIAL).
REPEAT	413	PRT	CARBOHYD	1518	1518	N-LINKED (GLCNAC. . .) (POTENTIAL).
REPEAT	657	PRT	CARBOHYD	1523	1523	N-LINKED (GLCNAC. . .) (POTENTIAL).
REPEAT	1092	PRT	CARBOHYD	1641	1641	N-LINKED (GLCNAC. . .) (POTENTIAL).
REPEAT	1415	PRT	CARBOHYD	2222	AA;	DF6452A2175C6B19 CRC64;
REPEAT	1678	PRT	SEQUENCE	252114	MW;	DF6452A2175C6B19 CRC64;
DOMAIN	1	IV.				
DOMAIN	40	IV.				
DOMAIN	41	IV.				
TRANSMEM	59	IV.				
TRANSMEM	60	IV.				
TRANSMEM	79	IV.				
TRANSMEM	98	IV.				
TRANSMEM	110	IV.				
TRANSMEM	124	IV.				
TRANSMEM	125	IV.				
TRANSMEM	136	IV.				
TRANSMEM	137	IV.				
TRANSMEM	156	IV.				
TRANSMEM	157	IV.				
TRANSMEM	174	IV.				
TRANSMEM	195	IV.				
TRANSMEM	277	IV.				
TRANSMEM	278	IV.				
TRANSMEM	301	IV.				
TRANSMEM	427	IV.				
TRANSMEM	428	IV.				
TRANSMEM	448	IV.				
TRANSMEM	461	IV.				
TRANSMEM	480	IV.				
TRANSMEM	490	IV.				
TRANSMEM	508	IV.				
TRANSMEM	518	IV.				
TRANSMEM	519	IV.				
TRANSMEM	538	IV.				
TRANSMEM	557	IV.				
TRANSMEM	576	IV.				
TRANSMEM	629	IV.				
TRANSMEM	630	IV.				
TRANSMEM	654	IV.				
TRANSMEM	655	IV.				
TRANSMEM	1101	IV.				
TRANSMEM	1117	IV.				
TRANSMEM	1141	IV.				
TRANSMEM	1142	IV.				
TRANSMEM	1161	IV.				
TRANSMEM	1169	IV.				
TRANSMEM	1192	IV.				
TRANSMEM	1193	IV.				
TRANSMEM	1206	IV.				
TRANSMEM	1207	IV.				
TRANSMEM	1224	IV.				
TRANSMEM	1225	IV.				
TRANSMEM	1243	IV.				
TRANSMEM	1451	IV.				
TRANSMEM	1467	IV.				
TRANSMEM	1468	IV.				
TRANSMEM	1493	IV.				
TRANSMEM	1494	IV.				
TRANSMEM	1512	IV.				
TRANSMEM	1513	IV.				
TRANSMEM	1523	IV.				
TRANSMEM	1524	IV.				
TRANSMEM	1542	IV.				
TRANSMEM	1543	IV.				
TRANSMEM	1561	IV.				
TRANSMEM	1562	IV.				
TRANSMEM	1581	IV.				
TRANSMEM	1650	IV.				
TRANSMEM	1651	IV.				
TRANSMEM	1676	IV.				
TRANSMEM	1677	IV.				
TRANSMEM	2272	IV.				
TRANSMEM	667	IV.				
TRANSMEM	699	IV.				
TRANSMEM	704	IV.				
TRANSMEM	723	IV.				
TRANSMEM	723	IV.				
POLY-ARG.	723	IV.				
POLY-ARG.	1058	IV.				
POLY-VAL.	1180	IV.				
POLY-VAL.	1183	IV.				
POLY-VAL.	2193	IV.				
POLY-VAL.	2196	IV.				
BINDING TO THE BETA SUBUNIT (BY SIMILARITY).	325	IV.				
BINDING TO THE BETA SUBUNIT (BY SIMILARITY).	342	IV.				
CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).	260	IV.				
CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).	608	IV.				
CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).	1324	IV.				
Query Match				18	78;	Score 65.5;
Best Local Similarity				32.4 %;	Pred. No. 34;	
Matches				9;	Mismatches	24;
					Indels	15;
					Gaps	
QY	3	Db	DNSHHIGGKRSQCVR-RCEDDRPHWRPCLQECDEER-----EKROERS---R	48	1977	DSGHSSDTTHSGGRERK-HILSDPVDSRNSSENGTQADWESPQRQSSECR 2035
QY	49	Db	HEADDGGEGS	59	2036	SQTPNQGIGS 2046
RESULT	15					
CCAE_MOUSE						
ID	CCAE_MOUSE					
AC	061240;					
DT	15-JUL-1999	(rel.	38,	Created)		
DT	30-MAY-2000	(rel.	39,	Last annotation update)		
DT	VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE, ISOFORM 6	(BRAIN CALCIUM CHANNEL 1) (BII).				
RC	CACNA1E OR CCHRA1 OR CACNL1A6 OR CACH6.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=BALB/C; TISSUE=Brain;					
RL	J. Biol. Chem. 269:2347-2357(1994).					
RA	Williams M.E., Marubio L.M., Deal C.R., Hans M., Brust P.F., Philipson L.H., Miller R.J., Johnson E.C., Harpold M.M., Ellis S.B.;					
RA	"Structure and functional characterization of neuronal alpha 1E calcium channel subtypes";					
CC	MEIDLINE=435092; PubMed=8071363;					
CC	ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MITOSIS, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1E GIVES RISE TO R-TYPE CALCIUM CURRENTS. R-TYPE CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP AND ARE BLOCKED BY NICKEL, AND PARTIALLY BY OMEGA-AGATOXIN-1IA (OMEGA-AGA-1IA). THEY ARE, HOWEVER, PARTIALLY SENSITIVE TO DIHYDROPIRIDINES (DHP), OMEGA-CONOTOXIN-GVIA (OMEGA-CTTX-GVIA), AND OMEGA-AGATOXIN-1VA (OMEGA-AGA-1VA). CALCIUM CHANNELS CONTAINING ALPHA-1E SUBUNIT COULD BE INVOLVED IN THE MODULATION OF FIRING PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING.					
CC	-!- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.					
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.					
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL TISSUES, RETINA, SPLEEN, AND PANCREATIC ISLET CELLS.					
CC	-!- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE					

CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.
 CC -!- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS
 CC FAMILY.
 CC
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 DR EMLB; L29346; AAA59205; 1; -.
 DR MGD; MGII:106217; CACNAE.
 DR INTERPRO; IPR00033; .
 DR INVERPRO; IPR002077; -.
 DR PFAM; PF00520; ion_trans; 4.
 DR PRINTS; PROJ167; CACHANEL.
 KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
 KW Calcium-binding; Glycoprotein; Repeat; Multigene family;
 KW Calcium-binding; Phosphorylation.
 FT REPEAT 77 355 I.
 FT REPEAT 463 707 II.
 FT REPEAT 1143 1429 III.
 FT DOMAIN 1466 1729 IV.
 FT DOMAIN 1 90 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 91 109 S1 OF REPEAT I (POTENTIAL).
 FT DOMAIN 110 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 147 S2 OF REPEAT I (POTENTIAL).
 FT DOMAIN 148 159 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 169 174 S3 OF REPEAT I (POTENTIAL).
 FT DOMAIN 175 186 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 187 206 S4 OF REPEAT I (POTENTIAL).
 FT DOMAIN 207 224 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 225 245 S5 OF REPEAT I (POTENTIAL).
 FT DOMAIN 246 327 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 328 351 S6 OF REPEAT I (POTENTIAL).
 FT DOMAIN 352 397 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 478 497 S1 OF REPEAT II (POTENTIAL).
 FT DOMAIN 498 510 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 511 530 S2 OF REPEAT II (POTENTIAL).
 FT DOMAIN 531 559 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 540 558 S3 OF REPEAT II (POTENTIAL).
 FT DOMAIN 559 568 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 569 587 S4 OF REPEAT II (POTENTIAL).
 FT DOMAIN 588 606 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 607 625 S5 OF REPEAT II (POTENTIAL).
 FT DOMAIN 627 679 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 680 704 S6 OF REPEAT II (POTENTIAL).
 FT DOMAIN 705 1150 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1151 1167 S1 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1168 1191 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1192 1211 S2 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1212 1219 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1240 1242 S3 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1243 1256 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1257 1274 S4 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1275 1293 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1294 1313 S5 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1314 1400 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1401 1424 S6 OF REPEAT III (POTENTIAL).
 FT DOMAIN 1425 1481 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1482 1500 S1 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1501 1515 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1516 1535 S2 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1536 1543 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1544 1562 S3 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1563 1573 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1574 1592 S4 OF REPEAT IV (POTENTIAL).
 FT DOMAIN 1593 1611 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1612 1631 S5 OF REPEAT IV (POTENTIAL).

FT	DOMAIN	1632	1700	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1701	1726	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1727	2272	CYTOSLAMIC (POTENTIAL).
FT	DOMAIN	717	722	POLY-GLU.
FT	DOMAIN	751	754	POLY-ARG.
FT	DOMAIN	770	773	POLY-GLU.
FT	DOMAIN	1108	1112	POLY-LYS.
FT	DOMAIN	1115	1118	POLY-VAL.
FT	DOMAIN	1231	1234	POLY-ARG.
FT	DOMAIN	2244	2247	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	DOMAIN	375	392	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	310	310	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	658	658	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1375	1375	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	SITE	1666	1666	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	CA_BIND	427	439	BY SIMILARITY.
FT	MOD_RES	1737	1737	PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT	CA_BIND	1755	1766	BY SIMILARITY.
FT	CARBHYD	255	255	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBHYD	1569	1569	N-LINKED (GLCNAC. . .) (POTENTIAL);
FT	CARBHYD	1692	257	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	2272	AA;	MW: 70D920B9EC0C87A1 CRC4:

Query	Match	Score	DB	Length
Best Local Matches	Similarity 23; Conservative 9; Mismatches 24;	32.4%	Pred.	No. 35;
Qy	DNHHHHGGHSGQCYR-RCHDRPWHQRPRCQEERER-----ERQERS---R	18.7%	Indels	15;
Db	DSGHKSDTHRSGRERGRSERR-LLSPDVSRCNSEERGTOADWESPERQSRSPSEGHR	32.4%	Gaps	4;
Qy	49 HEADERSGEES 59			
Db	2087 SQTTPNRQGTGS 2097			